GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 21:41:17 ; Search time 80 Seconds
              (without alignments)
              49.430 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*

```
1: genesecp1980s:*
2: genesecp1990s:*
3: genesecp2000s:*
4: genesecp2001s:*
5: genesecp2002s:*
6: genesecp2003as:*
7: genesecp2003bs:*
8: genesecp2004s:*
9: genesecp2005s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	2	AAW99196	Aaw99196 Minor his
2	45	100.0	9	2	AAW97375	Aaw97375 HA-1 H-al
3	45	100.0	9	8	ADH40333	Adh40333 Human min
4	45	100.0	13	2	AAW99199	Aaw99199 VR cell K
5	45	100.0	13	8	AAW97415	Aaw97415 KIAA0223
6	45	100.0	1165	8	ADS11768	Ads11768 Human the
7	38	84.4	199	2	ADF06830	Adf06830 Bacterial
8	37	82.2	9	2	AAW99197	Aaw99197 Minor his
9	37	82.2	9	2	AAW97374	Aaw97374 HA-1 R-al
10	37	82.2	9	2	AAW99374	Aaw99374 HA-1 R-al
11	37	82.2	9	2	ADH40334	Adh40334 Human min
12	37	82.2	13	2	AAW99198	Aaw99198 DH cell K
13	37	82.2	13	2	AAW97414	Aaw97414 KIAA0223
14	37	82.2	13	2	AAW99198	Aaw99198 KIAA0223
15	37	82.2	1136	8	ADI17193	Adi17193 Human NOV
16	37	82.2	1136	8	ADI16744	Adi16744 Human NOV
17	37	82.2	1136	8	ADH61299	Adh61299 INISIG pr
18	37	82.2	1136	8	ADH42398	Adh42398 Human nov
19	37	82.2	1165	8	ADS10490	Ads10490 Human the
20	37	82.2	1165	5	ADI17194	Adi17194 Human NOV
21	37	82.2	1165	8	ADP55035	Adp55035 Human PRO
22	36	80.0	9	2	ADP24600	Adp24600 PRO polyp
23	36	80.0	9	2	AAW99195	Aaw99195 Minor his
24	35	77.8	148	8	AAW97572	Aaw97572 T-cell ep
25	35	77.8	608	7	ABO77464	Abo77464 Pseudomon
26	35	77.8	786	7	ABU29875	Abu29875 Protein e
27	35	77.8	786	9	ADV16669	Adv16669 E. faeciu
28	35	77.8	789	7	ADC97107	Adc97107 B. faeciu
29	35	77.8	964	6	ADB70281	Adb70281 C. neofor
30	34	75.6	130	6	ABU26589	Abu26589 Protein e
31	34	75.6	130	9	AEA22128	Aea22128 Campyloba
32	34	75.6	232	4	AAU55593	Aau55593 Propionib
33	34	75.6	232	6	ABM52112	Abm52112 Propionib
34	34	75.6	253	6	ABU42064	Abu42064 Protein e
35	34	75.6	332	6	ABB64157	Abb64157 Drosophil
36	34	75.6	385	4	ABU41832	Abu41832 Protein e
37	34	75.6	440	4	AAB74623	Aab74623 Saitoella
38	34	75.6	446	8	ABU34950	Abu34950 Protein e
39	34	75.6	554	6	ADY09404	Ady09404 Plant ful
40	34	75.6	680	8	ADJ48425	Adj48425 Maize oil
41	34	75.6	774	8	ABB65640	Abb65640 Drosophil
42	34	75.6	774	4	AAU38963	Aau38963 Drosophil
43	34	75.6	774	7	ADC35871	Adc35871 Drosophil
44	34	75.6	783	4	AAG91263	Aag91263 C glutami
45	34	75.6	802	7	AAE38199	Aae38199 Fruit fly

ALIGNMENTS

RESULT 1
AAW99196

```
ID   AAW99196 standard; peptide; 9 AA.
XX
AC   AAW99196;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;  98WO-NL000425.
XX
PR   23-JUL-1997;  97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Claim 3; Page 32; 47pp; English.
XX
CC   The present sequence represents a new peptide (p1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases.
XX
SQ   Sequence 9 AA;
```

Qy   1 VLHDDLLEA 9
            |||||||||
Db   1 VLHDDLLEA 9

RESULT 2
ID   AAW97375
AC   AAW97375;
DT   13-MAY-1999 (first entry)
DE   HA-1 H-allele sequence.
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
OS   Homo sapiens.
PN   WO9905313-A2.
PD   04-FEB-1999.
PF   23-JUL-1998; 98WO-EP004928.
PR   23-JUL-1997; 97EP-00202303.
PR   02-JUN-1998; 98EP-0087O125.
PA   (UYLE-) RIJKSUNIV LEIDEN.
PI   Goulmy B;
DR   WPI; 1999-142960/12.
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
PS   Claim 18; Fig 5; 59pp; English.
CC   The present sequence represents part of the minor histocompatibility
CC   antigen HA-1 H-allele. The specification describes methods for typing
CC   alleles (preferably the H which R alleles) of the minor histocompatibility
CC   antigen HA-1 in a sample, which comprise detecting polymorphic
CC   nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC   methods can be used for HA-1 typing for bone marrow transplants, severe
CC   aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC   detection of genetic aberrances. The probes and primers of the invention
CC   can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC   anti-idiotypic B cells and/or T cells and antibodies
SQ   Sequence 9 AA;

Query Match   100.0%; Score 45; DB 2; Length 9;
Best Local Similarity   100.0%; Pred. No. 2e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
            |||||||||
Db   1 VLHDDLLEA 9

RESULT 3
ID   ADH40333
AC   ADH40333;
ID   ADH40333 standard; peptide; 9 AA.

XX
DT   11-MAR-2004 (first entry)
DE   Human minor histocompatibility antigen HA-1 T cell epitope.
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocompatibility antigen; mHAg; T cell epitope.
OS   Homo sapiens.
PN   WO200310692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
PR   13-JUN-2002; 2002EP-00013423.
PA   (MERE) MERCK PATENT GMBH.
PI   Strittmatter W, Moll H;
DR   WPI; 2004-082200/08.
PS   Disclosure; Page 82; 119pp; English.
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
SQ   Sequence 9 AA;

Query Match   100.0%; Score 45; DB 8; Length 9;
Best Local Similarity   100.0%; Pred. No. 2e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
            |||||||||
Db   1 VLHDDLLEA 9

RESULT 4
ID   AAW99199
AC   AAW99199;
ID   AAW99199 standard; peptide; 13 AA.
DT   20-MAY-1999 (first entry)
DE   VR cell KIAA0223 protein sequence.
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 21:41:50 ; Search time 16 Seconds
                              (without alignments)
                              54.122 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLIEA 9
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR 80:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	84.4	1148	2	S51855	hypothetical prote
2	37	82.2	1165	2	D59433	C. elegans protein
3	35	77.8	119	2	T00151	hypothetical prote
4	35	77.8	604	2	S36487	E1 protein - human
5	35	77.8	605	2	S36469	E1 protein - human
6	35	77.8	616	2	C69226	type I restriction
7	34	75.6	130	2	A81316	chemotaxis regulat
8	33	73.3	145	2	A41652	probable glyceroph
9	33	73.3	174	2	C89075	protein K04A8.9 [1
10	33	73.3	210	2	T44122	probable glyceroph
11	33	73.3	210	2	E89762	hypothetical prote
12	33	73.3	238	2	S76860	hypothetical prote
13	33	73.3	249	2	AG0461	glycerophosphodies
14	33	73.3	259	2	G82601	conserved hypothet
15	33	73.3	291	2	D83371	probable dehydroge
16	33	73.3	320	2	B75457	polyprenyl synthas
17	33	73.3	322	2	C83075	octaprenyl-diphosp
18	33	73.3	343	2	A1058I	DNA polymerase III
19	33	73.3	343	2	B85564	DNA polymerase III
20	33	73.3	343	2	P90713	DNA polymerase III
21	33	73.3	343	2	A42251	DNA-directed DNA p
22	33	73.3	378	2	T3540I	probable polypreny
23	33	73.3	397	2	S09813	hypothetical prote
24	33	73.3	398	2	H72660	probable N-Acylami
25	33	73.3	519	2	S69988	unspecific monooxy
26	33	73.3	519	2	S69989	unspecific monooxy
27	33	73.3	604	2	S36493	E1 protein - human
28	33	73.3	654	2	AH0668	probable peptidase
29	33	73.3	667	2	G90883	probable collagena
30	33	73.3	667	2	H85734	probable collagena
31	33	73.3	667	2	F64895	hypothetical prote
32	33	73.3	723	2	F85047	hypothetical prote
33	33	73.3	856	2	C85023	hypothetical prote
34	33	73.3	908	2	T50695	secA protein [impo
35	33	73.3	973	2	T50449	DNA repair and rec
36	33	73.3	1127	2	S47445	MDM1 protein - yea
37	33	73.3	1770	1	S56221	ribonuclease inhib
38	32	71.1	91	1	C69973	acidic ribosomal P
39	32	71.1	107	1	R6KM1C	A-ORF-B protein -
40	32	71.1	166	2	A42524	hypothetical prote
41	32	71.1	270	2	G84226	hypothetical prote
42	32	71.1	276	2	T28746	hypothetical prote
43	32	71.1	284	2	G70732	probable thiosulfa
44	32	71.1	296	2	T27768	hypothetical prote
45	32	71.1	297	2	A84759	probable trans-pre

ALIGNMENTS

RESULT 1
S51855
hypothetical protein YDR128w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9302.03
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
C;Accession: S51855
R;Oliver, K.; Harris, D.
submitted to the EMBL Data Library, February 1995
A;Reference number: S51853
A;Gene: MIPS:YDR128w
A;Accession: S51855
A;Molecule type: DNA
A;Residues: 1-1148 <OLI>
A;Cross-references: UNIPROT:O03897; UNIPARC:UPI000006A370; EMBL:Z48179; NID:g665657; PII
C;Genetics:
A;Gene: MIPS:YDR128w
A;Cross-references: SGD:S0002535
A;Map position: 4R

Query Match		84.4%;							
Best Local Similarity		66.7%;							
Matches	6;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;

Qy   1 VLHDDLIEA 9
            :||||||::||
Db   1001 LLHDDIERA 1009

RESULT 2
D59433
C. elegans protein Z37093 homolog [imported] - human
C;Species: Homo sapiens (man)
C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C;Accession: D59433; E59433
R;Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.; Ohara, O.; Tanaka, A.
DNA Res. 3, 321-329, 1996
A;Title: Prediction of the coding sequences of unidentified human genes. VI. The coding
A;Reference number: D59433; MUID:97191544; PMID:9039502
A;Accession: D59433
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1165 <NAG>
A;Cross-references: UNIPROT:Q92619; UNIPARC:UPI000007BEAF; GB:BAA13212; PID:g1504026; PI
R;Ohara, O.; Nagase, T.; Kikuno, R.; Nomura, N.
submitted to Genbank, August 1996
A;Reference number: E59433
A;Accession: E59433
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1165 <STO2>
A;Cross-references: UNIPARC:UPI000007BEAF; GB:BAA13212; PID:g1504026; PIDN:BAA13212.1

Qy
Db

```
Query Match                82.2%;  Score 37;  DB 2;  Length 1165;
Best Local Similarity      88.9%;  Pred. No. 82;
Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

       1 VLHDDLLEA 9
         ||||||||
     166 VLRDDLLEA 174
```

RESULT 3
T00151
hypothetical protein 18 - Staphylococcus aureus phage phi PVL
C;Species: Staphylococcus aureus phage phi PVL
C;Accession: T00151
R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997
A;Title: Panton-Valentine leukocidin genes in a phage-like particle isolated from mitomy
A;Reference number: Z14119; MUID:98067870; PMID:9404084
A;Accession: T00151
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reference number: S36469
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Cross-references: UNIPROT:O80057; UNIPARC:UPI00009AFCD; EMBL:AB009866; NID:g33341907;
A;Superfamily: Staphylococcus aureus phage phi PVL hypothetical protein 18

```
Query Match                77.8%;  Score 35;  DB 2;  Length 119;
Best Local Similarity      85.7%;  Pred. No. 15;
Matches      6;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;
```

Qy
Db

```
       3 HDDLLEA 9
         |||:||||
      72 HDDLLEA 78
```

RESULT 4
S36487
E1 protein - human papillomavirus type 19
C;Species: human papillomavirus type 19
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36487
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36487
A;Molecule type: DNA
A;Residues: 1-604 <DEL>
A;Cross-references: UNIPROT:Q02048; UNIPARC:UPI00001382P0; EMBL:X74470; NID:g3396940; PID
A;Superfamily: papillomavirus E1 protein
C;Keywords: early protein; nucleus

```
Query Match                77.8%;  Score 35;  DB 2;  Length 604;
Best Local Similarity      75.0%;  Pred. No. 94;
Matches      6;  Conservative      2;  Mismatches      0;  Indels      0;  Gaps      0;
```

Qy
Db

```
       2 LHDDLLEA 9
         ||||||||:
     201 VHDDLLES 208
```

RESULT 5
S36469
E1 protein - human papillomavirus type 14D
C;Species: human papillomavirus type 14D
C;Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S36469
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36469

A;Molecule type: DNA
A;Residues: 1-605 <DEL>
A;Cross-references: UNIPROT:P36721; UNIPARC:UPI00001382EC; EMBL:X74467; NID:g3396918; PID
A;Experimental source: strain 14D
A;Superfamily: papillomavirus E1 protein
C;Keywords: early protein; nucleus

```
Query Match                77.8%;  Score 35;  DB 2;  Length 605;
Best Local Similarity      75.0%;  Pred. No. 94;
Matches      6;  Conservative      2;  Mismatches      0;  Indels      0;  Gaps      0;
```

Qy
Db

```
       2 LHDDLLEA 9
         ||||||||:
     202 VHDDLLES 209
```

RESULT 6
C69226
type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69226
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69226
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-616 <MTH>
A;Cross-references: UNIPROT:O27025; UNIPARC:UPI000066673D; GB:AB000868; GB:AE000666; NID
A;Experimental source: strain Delta H
A;Genetics:
A;Gene: MTH942
A;Start codon: GTG
A;Superfamily: type I site-specific deoxyribonuclease chain hsdM

```
Query Match                77.8%;  Score 35;  DB 2;  Length 616;
Best Local Similarity      77.8%;  Pred. No. 96;
Matches      7;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;
```

Qy
Db

```
       1 VLHDDLLEA 9
         || ||||:||
     465 VLEDDLLEA 473
```

RESULT 7
A81316
chemotaxis regulatory protein Cj1118c [imported] - Campylobacter jejuni (strain NCTC 111
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: A81316
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: A81316
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-130 <PAR>
A;Cross-references: UNIPROT:P71129; UNIPARC:UPI000012770; GB:AL139077; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
A;Genetics:
A;Gene: cheY; Cj1118c
A;Superfamily: signal transduction receiver (phosphoacceptor) protein, CheY type; respon

```
Query Match                75.6%;  Score 34;  DB 2;  Length 130;
Best Local Similarity      85.7%;  Pred. No. 26;
Matches      6;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;
```

OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Biocceleration Ltd.

GenCore version 5.1.7

Run on: March 2, 2006, 21:41:26 ; Search time 72 seconds
(without alignments)
88.191 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLRA 9

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Scoring table: BLOSUM62

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	1136	2	Q6P189_HUMAN	homo sapien
2	40	88.9	571	2	Q6KZH5_PICTO	picrophilus
3	39	86.7	668	2	Q6LZ81_METMP	methanococc
4	38	84.4	1148	2	O03897_YEAST	saccharomyc
5	38	84.4	1176	2	Q5CSZ8_CRYPV	cryptospori
6	37	82.2	1131	2	Q8IYN3_HUMAN	homo sapien
7	37	82.2	1136	2	Q8HX84_HUMAN	homo sapien
8	37	82.2	1163	2	Q5RB40_PONPY	pongo pygma
9	37	82.2	1165	2	Q92619_HUMAN	homo sapien
10	36	80.0	101	2	Q6AMV9_DESPS	desulfotale
11	36	80.0	231	2	Q6AUN7_ORYSA	oryza sativ
12	36	80.0	253	2	Q4ZMT6_PSESY	pseudomonas
13	36	80.0	585	2	Q8EJS9_SHEON	shewanella
14	36	80.0	691	2	Q8PQR0_XANAC	xanthomonas
15	36	80.0	694	2	Q5GU33_XANOR	xanthomonas
16	36	80.0	870	2	Q5QUQ7_IDILO	idiomarina
17	36	80.0	1155	2	Q4PCT0_USTMA	ustilago ma
18	35	77.8	119	2	Q8O057_9CAUD	staphylococ
19	35	77.8	120	2	Q8SCW6_9CAUD	pseudomonas
20	35	77.8	148	2	Q62W54_9CAUD	homo sapien
21	35	77.8	268	2	Q4FUQ3_9GAMM	psychrobact
22	35	77.8	354	2	Q57ZU0_9TRYP	trypanosoma
23	35	77.8	376	2	Q8MVB1_IXOSC	ixodes scap
24	35	77.8	415	2	Q4Q35_LEIMA	leishmania
25	35	77.8	415	2	Q5GAQ4_MAIZE	zea mays (m
26	35	77.8	415	2	Q5GAU2_MAIZE	zea mays (m
27	35	77.8	496	2	Q8SDK3_BPPHD	bacteriopha
28	35	77.8	496	2	Q9MBP0_9CAUD	staphylococ
29	35	77.8	579	2	Q5Y41_NOCFA	nocardia fa
30	35	77.8	579	2	Q5ND23_TETNG	tetraodon n
31	35	77.8	590	2	Q5NDE4_FUGRU	fugu rubrip
32	35	77.8	603	1	VB1_HPV21	human papil	P50759 human papil
33	35	77.8	604	1	VB1_HPV19	human papil	Q02048 human papil
34	35	77.8	605	1	VB1_HPV14	human papil	P36721 human papil
35	35	77.8	616	2	O27025_METTH	methanobact	O27025 methanobact
36	35	77.8	843	2	Q52KE4_CHICK	gallus gall	Q52ke4 gallus gall
37	35	77.8	843	2	Q8JH28_CHICK	gallus gall	Q8jh28 gallus gall
38	35	77.8	872	2	Q6DIR8_XENTR	xenopus tro	Q6dir8 xenopus tro
39	35	77.8	952	2	Q5KDU2_CRYNE	cryptococcu	Q5kdu2 cryptococcu
40	35	77.8	952	2	Q5SPL4_CRYNE	cryptococcu	Q5spl4 cryptococcu
41	35	77.8	1246	2	Q4QHU5_LEIMA	leishmania	Q4qhu5 leishmania
42	34	75.6	68	2	Q5SPL4_LEPIN	leptospira	Q8eyr5 leptospira
43	34	75.6	113	2	Q53NG1_ORYSA	oryza sativ	Q53ng1 oryza sativ
44	34	75.6	130	1	Q8EYR5_LEPIN	leptospira	Q71129 campylobact
45	34	75.6	130	2	Q5HTY6_CAMJR	campylobact	Q5hty6 campylobact

ALIGNMENTS

RESULT 1
Q6P189_HUMAN
Q6P189_HUMAN PRELIMINARY;   PRT;   1136 AA.
ID   Q6P189_HUMAN PRELIMINARY;   PRT;   1136 AA.
AC   Q6P189;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Minor histocompatibility antigen HA-1.
GN   Name=HA-1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC065223; AAH65223.1; -; mRNA.
DR   HSSP; Q07960; 1AM4.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   InterPro; IPR001060; Cdc15 Fes_CIP4.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000198; RhoGAP.
DR   InterPro; IPR000130; C1.
DR   Pfam; PF00620; RhoGAP; 1.
DR   Pfam; PF00130; C1_1; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00055; FCH; 1.

DR   SMART; SM00324; RhoGAP; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR   PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50238; RHOGAP; 1.
SQ   SEQUENCE 1136 AA; 124450 MW; 14B70732961D2DD5 CRC64;

Qy   Score 45; DB 2; Length 1136;
Best Local Similarity   100.0%;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
         |||||||||
Db   137 VLHDDLLEA 145

RESULT 2
Q6KZH5_PICTO
ID   Q6KZH5_PICTO PRELIMINARY;   PRT;   571 AA.
AC   Q6KZH5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Molybdopterin biosynthesis MoeA protein.
GN   OrderedLocusNames=PTO1292;
OS   Picrophilus torridus.
OC   Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC   Picrophilaceae; Picrophilus.
OX   NCBI_TaxID=82076;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DSM 9790 / ATCC 700027;
RX   PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA   Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA   Schepers B., Dock C., Antranikian G., Liebl W.;
RT   "Genome sequence of Picrophilus torridus and its implications for life
RT   around pH 0.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR   EMBL; AE017261; AAT43877.1; -; Genomic_DNA.
DR   GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR   InterPro; IPR001453; MoeA_bios.
DR   InterPro; IPR005111; MoeA_C.
DR   InterPro; IPR005110; MoeA_N.
DR   Pfam; PF00994; MoCF_biosynth; 1.
DR   Pfam; PF03454; MoeA_C; 1.
DR   Pfam; PF03453; MoeA_N; 1.
DR   ProDom; PD002460; MoCF_biosynth; 1.
DR   TIGRFAMs; TIGR00177; molyb_syn; 1.
KW   Complete proteome.
SQ   SEQUENCE 571 AA; 64707 MW; D2EB18FBFC115FA1 CRC64;

Query Match
Best Local Similarity   88.9%;   Score 40; DB 2; Length 571;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
        ||||||| |
Db   63 VLHDDLLNA 71

RESULT 3
Q6LZ81_METMP
ID   Q6LZ81_METMP PRELIMINARY;   PRT;   668 AA.
AC   Q6LZ81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MCM family related protein.
GN   OrderedLocusNames=MMP0748;
OS   Methanococcus maripaludis.
OC   Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC   Methanococcaceae; Methanococcus.
OX   NCBI_TaxID=39152;
RN   [1]

RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=S2 / LL;
RX   PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004;
RA   Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
RA   Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E.,
RA   Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
RA   Major T.A., Moore B.C., Porat I., Palmeiri A., Rouse G.,
RA   Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B.,
RA   Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
RT   "Complete genome sequence of the genetically tractable
RT   hydrogenotrophic methanogen Methanococcus maripaludis.";
RL   J. Bacteriol. 186:6956-6969(2004).
DR   EMBL; BX957221; CAF30304.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0008094; F:DNA-dependent ATPase activity; IEA.
DR   GO; GO:0006270; P:DNA replication initiation; IEA.
DR   InterPro; IPR001208; MCM.
DR   Pfam; PF00493; MCM; 1.
DR   PRINTS; PR01657; MCMFAMILY.
DR   ProDom; PD001041; MCM; 1.
DR   SMART; SM00350; MCM; 1.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR   PROSITE; PS00017; MCM_1.
DR   PROSITE; PS50051; MCM_2; 1.
KW   Complete proteome.
SQ   SEQUENCE 668 AA; 75660 MW; 2ADAF3800B1049F4 CRC64;

Query Match
Best Local Similarity   86.7%;   Score 39; DB 2; Length 668;
Matches   8; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
         ||||||||
Db   628 VLHDDLLEA 636

RESULT 4
Q03897_YEAST
ID   Q03897_YEAST PRELIMINARY;   PRT;   1148 AA.
AC   Q03897;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=YDR128W;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB972;
RA   Oliver K., Harris D.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB972;
RA   Barrell B., Rajandream M.A.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- INTERACTION:
CC   P39079:CCT6; NbExp=1; IntAct=EBI-32422, EBI-19077;
DR   EMBL; Z48179; CAA88209.1; -; Genomic_DNA.
DR   PIR; S51855; S51855.
DR   IntAct; Q03897;
DR   Ensembl; YDR128W; Saccharomyces cerevisiae.
DR   SGD; S000002535; YDR128W.
DR   GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
DR   InterPro; IPR006575; RWD.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 4.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   SMART; SM00591; RWD; 1.

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: March 2, 2006, 21:42:32 ; Search time 17 seconds
                                (without alignments)
                                43.769 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database :   Issued_Patents_AA:*
   1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
   2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
   3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
   4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
   5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
   6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	45	100.0	9	2	US-09-269-250B-20	Sequence 20, Appli
2	45	100.0	9	2	US-09-489-760-2	Sequence 2, Appli
3	45	100.0	13	2	US-09-269-250B-28	Sequence 28, Appl
4	45	100.0	13	2	US-09-489-760-16	Sequence 16, Appl
5	45	100.0	26	2	US-09-269-250B-36	Sequence 36, Appl
6	38	84.4	199	2	US-09-543-681A-7115	Sequence 7115, Ap
7	38	84.4	1148	2	US-09-538-092-156	Sequence 156, App
8	37	82.2	9	2	US-09-269-250B-18	Sequence 18, Appl
9	37	82.2	9	2	US-09-489-760-5	Sequence 5, Appl
10	37	82.2	13	2	US-09-269-250B-26	Sequence 26, Appl
11	37	82.2	13	2	US-09-489-760-14	Sequence 14, Appl
12	36	80.0	9	2	US-09-269-250B-29	Sequence 29, Appl
13	36	80.0	9	2	US-09-489-760-1	Sequence 1, Appl
14	35	77.8	608	2	US-09-252-991A-26210	Sequence 26210, A
15	35	77.8	789	2	US-09-107-532A-6734	Sequence 6734, Ap
16	34	75.6	435	2	US-09-270-767-33480	Sequence 33480, A
17	34	75.6	435	2	US-09-270-767-48697	Sequence 48697, A
18	34	75.6	446	2	US-09-830-111B-2	Sequence 2, Appl
19	33	73.3	70	2	US-09-134-000C-3701	Sequence 3701, Ap
20	33	73.3	256	2	US-09-134-001C-4544	Sequence 4544, Ap
21	33	73.3	295	2	US-09-252-991A-24727	Sequence 24727, A
22	33	73.3	332	2	US-09-902-540-12129	Sequence 12129, A
23	33	73.3	341	2	US-09-252-991A-21448	Sequence 21448, A
24	33	73.3	342	2	US-09-818-780-97	Sequence 97, Appl
25	33	73.3	343	1	US-08-279-058B-9	Sequence 9, Appli
26	33	73.3	343	2	US-08-828-323-9	Sequence 9, Appli
27	33	73.3	343	2	US-08-828-323A-9	Sequence 9, Appli
28	33	73.3	352	2	US-09-489-039A-12951	Sequence 12951, A
29	33	73.3	623	2	US-09-710-279-1068	Sequence 1068, Ap
30	33	73.3	687	2	US-09-489-039A-9868	Sequence 9868, Ap
31	33	73.3	851	2	US-09-071-035-326	Sequence 326, App
32	33	73.3	851	2	US-09-071-035-330	Sequence 330, App
33	33	73.3	851	2	US-09-071-035-334	Sequence 334, App
34	33	73.3	851	2	US-10-206-576-326	Sequence 326, App
35	33	73.3	851	2	US-10-206-576-330	Sequence 330, App
36	33	73.3	851	2	US-10-206-576-334	Sequence 334, App
37	33	73.3	1554	2	US-09-252-991A-26814	Sequence 26814, A
38	33	73.3	1770	2	US-09-487-558B-298	Sequence 298, App
39	33	73.3	4150	2	US-09-428-517-2	Sequence 2, Appli
40	32	71.1	35	2	US-09-082-279B-454	Sequence 454, App
41	32	71.1	35	2	US-09-082-279B-455	Sequence 455, App
42	32	71.1	35	2	US-09-082-279B-456	Sequence 456, App
43	32	71.1	35	2	US-08-474-349A-481	Sequence 481, App
44	32	71.1	35	2	US-08-474-349A-482	Sequence 482, App
45	32	71.1	35	2	US-08-474-349A-483	Sequence 483, App

ALIGNMENTS

RESULT 1
US-09-269-250B-20

; Sequence 20, Application US/09269250B
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250B
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250B-20

Query Match   100.0%;   Score 45; DB 2; Length 9;
Best Local Similarity   100.0%;   Pred. No. 4.6e+05;
Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 VLHDDLLEA 9
        |||||||||
Db   1 VLHDDLLEA 9

RESULT 2
US-09-489-760-2

; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen

US-09-489-760-2

Qy
Db

Query Match
Best Local Similarity 100.0%;   Score 45;   DB 2;   Length 9;
Matches   9;   Conservative   0;   Pred. No. 4.6e+05;   Mismatches   0;   Indels   0;   Gaps   0;

```
1 VLHDDLLEA 9
  |||||||||
1 VLHDDLLEA 9
```

RESULT 3
US-09-269-250E-28
; Sequence 28, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28

Qy
Db

Query Match
Best Local Similarity 100.0%;   Score 45;   DB 2;   Length 13;
Matches   9;   Conservative   0;   Pred. No. 0.034;   Mismatches   0;   Indels   0;   Gaps   0;

```
1 VLHDDLLEA 9
  |||||||||
3 VLHDDLLEA 11
```

RESULT 4
US-09-489-760-16
; Sequence 16, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:HA-1+/+
US-09-489-760-16

Qy
Db

Query Match
Best Local Similarity 100.0%;   Score 45;   DB 2;   Length 13;
Matches   9;   Conservative   0;   Pred. No. 0.034;   Mismatches   0;   Indels   0;   Gaps   0;

```
1 VLHDDLLEA 9
  |||||||||
3 VLHDDLLEA 11
```

RESULT 5
US-09-269-250E-36
; Sequence 36, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 36
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-36

Qy
Db

Query Match
Best Local Similarity 100.0%;   Score 45;   DB 2;   Length 26;
Matches   9;   Conservative   0;   Pred. No. 0.072;   Mismatches   0;   Indels   0;   Gaps   0;

```
1 VLHDDLLEA 9
  |||||||||
16 VLHDDLLEA 24
```

RESULT 6
US-09-543-681A-7115
; Sequence 7115, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7115
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7115

Qy
Db

Query Match
Best Local Similarity 84.4%;   Score 38;   DB 2;   Length 199;
Matches   7;   Conservative   1;   Pred. No. 13;   Mismatches   1;   Indels   0;   Gaps   0;

```
1 VLHDDLLEA 9
  ||||||| :|
178 VLHDDLIRA 186
```

RESULT 7
US-09-538-092-156
; Sequence 156, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gioc, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965

```
OM protein - protein search, using sw model

                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Bioacceleration Ltd.

Run on:             March  2, 2006, 21:43:37 ; Search time 71 Seconds
                                               (without alignments)
                                               52.964 Million cell updates/sec

Title:              US-10-623-176A-2
Perfect score:      45
Sequence:           1 VLHDDLLEA 9
Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched:           1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:      1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published Applications AA Main:*
          1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
          2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
          3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
          4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
          5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
          6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	4	US-10-623-176-2	Sequence 2, Appli
2	45	100.0	9	4	US-10-791-217-2	Sequence 2, Appli
3	45	100.0	9	5	US-10-861-335-1	Sequence 1, Appli
4	45	100.0	9	4	US-11-007-740-20	Sequence 20, Appl
5	45	100.0	10	4	US-10-623-176-43	Sequence 43, Appl
6	45	100.0	13	4	US-10-623-176-76	Sequence 76, Appl
7	45	100.0	13	4	US-10-791-217-16	Sequence 16, Appl
8	45	100.0	13	6	US-11-007-740-28	Sequence 28, Appl
9	45	100.0	17	4	US-10-623-176-57	Sequence 57, Appl
10	45	100.0	22	4	US-10-623-176-53	Sequence 53, Appl
11	45	100.0	25	4	US-10-623-176-55	Sequence 55, Appl
12	45	100.0	26	6	US-11-007-740-36	Sequence 36, Appl
13	45	100.0	27	4	US-10-623-176-51	Sequence 51, Appl
14	45	100.0	29	4	US-10-623-176-49	Sequence 49, Appl
15	41	91.1	9	4	US-10-623-176-41	Sequence 41, Appl
16	41	91.1	9	4	US-10-623-176-47	Sequence 47, Appl
17	39	86.7	65	4	US-10-424-599-242306	Sequence 242306,
18	37	82.2	9	4	US-10-623-176-10	Sequence 10, Appl
19	37	82.2	9	4	US-10-791-217-5	Sequence 5, Appl
20	37	82.2	9	6	US-11-007-740-18	Sequence 18, Appl
21	37	82.2	9	4	US-10-623-176-44	Sequence 44, Appl
22	37	82.2	10	4	US-10-623-176-65	Sequence 65, Appl
23	37	82.2	12	4	US-10-623-176-65	Sequence 65, Appl
24	37	82.2	13	4	US-10-623-176-74	Sequence 74, Appl
25	37	82.2	13	4	US-10-791-217-14	Sequence 14, Appl
26	37	82.2	13	6	US-11-007-740-26	Sequence 26, Appl
27	37	82.2	17	4	US-10-623-176-69	Sequence 69, Appl
28	37	82.2	19	4	US-10-623-176-52	Sequence 52, Appl
29	37	82.2	19	4	US-10-623-176-70	Sequence 70, Appl
30	37	82.2	21	4	US-10-623-176-71	Sequence 71, Appl
31	37	82.2	22	4	US-10-623-176-63	Sequence 63, Appl
32	37	82.2	23	4	US-10-623-176-72	Sequence 72, Appl
33	37	82.2	25	4	US-10-623-176-67	Sequence 67, Appl
34	37	82.2	26	4	US-10-623-176-66	Sequence 66, Appl
35	37	82.2	27	4	US-10-623-176-60	Sequence 60, Appl
36	37	82.2	28	4	US-10-623-176-61	Sequence 61, Appl
37	37	82.2	29	4	US-10-072-012-280	Sequence 280, App
38	37	82.2	1136	4	US-10-072-012-729	Sequence 729, App
39	37	82.2	1136	4	US-10-072-012-730	Sequence 730, App
40	37	80.0	1165	4	US-10-623-176-1	Sequence 1, Appl
41	36	80.0	9	4	US-10-623-176-40	Sequence 40, Appli
42	36	80.0	9	4	US-10-791-217-1	Sequence 1, Appli
43	36	80.0	9	4	US-11-007-740-29	Sequence 29, Appl
44	36	80.0	9	6	US-10-623-176-6	Sequence 6, Appli
45	36	80.0	10	4		

ALIGNMENTS

```
RESULT 1
US-10-623-176-2

; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT:  Goulmy, Els A.J.M.
; APPLICANT:  Hunt, Donald F.
; APPLICANT:  Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE:  2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE:  2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE:  1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE:  1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE:  2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-2

  Query Match             100.0%;  Score 45;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 2
US-10-791-217-2

; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT:  Goulmy, Elsa A.J.M
; APPLICANT:  Hunt, Donald F
; APPLICANT:  Engelhard, Victor H
```

```
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE: 2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 2
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: Artificial sequence
;  FEATURE:
;  OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

Qy   1 VLHDDLLEA 9
       |||||||||
Db   1 VLHDDLLEA 9
```

```
Query Match           100.0%;   Score 45;  DB 4;  Length 9;
Best Local Similarity 100.0%;   Pred. No. 1.7e+06;
Matches   9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

US-10-791-217-2
```

```
RESULT 3
US-10-861-335-1
Sequence 1, Application US/10861335
;  Publication No. US20050031612A1
;  GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M.
;  TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
;  FILE REFERENCE: 2183-6479US
;  CURRENT APPLICATION NUMBER: US/10/861,335
;  CURRENT FILING DATE: 2004-06-04
;  PRIOR APPLICATION NUMBER: PCT/NL02/00791
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01204704.9
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 1
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

Qy   1 VLHDDLLEA 9
       |||||||||
Db   1 VLHDDLLEA 9
```

```
Query Match           100.0%;   Score 45;  DB 5;  Length 9;
Best Local Similarity 100.0%;   Pred. No. 1.7e+06;
Matches   9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

US-10-861-335-1
```

```
RESULT 4
US-11-007-740-20
Sequence 20, Application US/11007740
;  Publication No. US20050233350A1
;  GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE: 2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
```

```
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 20
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

Qy   1 VLHDDLLEA 9
       |||||||||
Db   1 VLHDDLLEA 9
```

```
Query Match           100.0%;   Score 45;  DB 6;  Length 9;
Best Local Similarity 100.0%;   Pred. No. 1.7e+06;
Matches   9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

US-11-007-740-20
```

```
RESULT 5
US-10-623-176-43
Sequence 43, Application US/10623176
;  Publication No. US20040092446A1
;  GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT: Hunt, Donald F.
;  APPLICANT: Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE: 2003-07-18
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 43
;  LENGTH: 10
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (1)..(10)
US-10-623-176-43

Qy   1 VLHDDLLEA 9
       |||||||||
Db   1 VLHDDLLEA 9
```

```
Query Match           100.0%;   Score 45;  DB 4;  Length 10;
Best Local Similarity 100.0%;   Pred. No. 0.17;
Matches   9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

US-10-623-176-43
```

```
RESULT 6
US-10-623-176-76
Sequence 76, Application US/10623176
;  Publication No. US20040092446A1
;  GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT: Hunt, Donald F.
;  APPLICANT: Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE: 2003-07-18
```

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: March 2, 2006, 21:44:02 ; Search time 12 seconds
(without alignments)
15.000 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Published Applications AA_New:*
1: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptcdata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptcdata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	45	100.0	9	7	US-11-010-748A-11	Sequence 11, Appl
2	37	82.2	9	7	US-11-010-748A-11	Sequence 12, Appl
3	33	73.3	519	7	US-11-087-099-5406	Sequence 5406, Ap
4	33	73.3	519	7	US-11-087-099-9352	Sequence 9352, Ap
5	33	73.3	623	6	US-10-793-626-1068	Sequence 1068, Appl
6	32	71.1	297	7	US-11-092-140-9	Sequence 9, Appli
7	32	71.1	321	7	US-11-092-140-12	Sequence 12, Appl
8	32	71.1	324	7	US-11-098-686-10760	Sequence 10760, A
9	32	71.1	422	6	US-11-524-647-122	Sequence 122, App
10	32	71.1	422	6	US-10-524-972-110	Sequence 110, App
11	32	71.1	442	6	US-10-485-788A-516	Sequence 516, Ap
12	32	71.1	580	7	US-11-072-512-2876	Sequence 2876, Ap
13	32	71.1	737	7	US-11-152-366-28	Sequence 28, Appl
14	32	71.1	226	6	US-10-510-941-20	Sequence 20, Appl
15	31	68.9	304	7	US-11-156-084-291	Sequence 291, Appl
16	31	68.9	310	7	US-11-156-084-301	Sequence 301, App
17	31	68.9	315	7	US-11-156-084-313	Sequence 313, App
18	31	68.9	315	7	US-11-156-084-353	Sequence 353, App
19	31	68.9	443	7	US-11-098-686-10861	Sequence 10861, A
20	31	68.9	469	7	US-11-124-368A-336	Sequence 336, App
21	31	68.9	469	7	US-11-124-368A-337	Sequence 337, App
22	31	68.9	1254	6	US-10-528-031-47	Sequence 47, Appl
23	31	68.9	1445	6	US-11-169-041-181	Sequence 181, Appl
24	31	68.9	4128	6	US-11-770-726-77	Sequence 77, Appl
25	31	68.9	4868	7	US-11-044-111-24	Sequence 24, Appl
26	30	66.7	139	7	US-11-087-099-7123	Sequence 7123, Ap
27	30	66.7	161	7	US-11-200-394-17	Sequence 17, Appl
28	30	66.7	345	7	US-11-087-099-3274	Sequence 3274, Ap
29	30	66.7	365	7	US-11-087-099-4866	Sequence 4866, Ap
30	30	66.7	386	7	US-11-087-099-12026	Sequence 12026, A
31	30	66.7	439	7	US-11-087-099-739	Sequence 739, App
32	30	66.7	439	7	US-11-087-099-2428	Sequence 2428, Ap
33	30	66.7	468	6	US-10-957-569-28	Sequence 28, Appl
34	30	66.7	468	6	US-11-097-589-26	Sequence 26, Appl
35	30	66.7	696	6	US-10-018-868-51	Sequence 51, Appl
36	30	66.7	1210	7	US-11-624-932-26	Sequence 26, Appl
37	30	66.7	1213	7	US-11-039-398-14	Sequence 14, Appl
38	30	66.7	1216	7	US-11-039-398-12	Sequence 12, Appl
39	30	66.7	1219	7	US-11-039-398-10	Sequence 10, Appl
40	30	66.7	1222	7	US-11-039-398-8	Sequence 8, Appli
41	30	66.7	1232	7	US-11-039-398-18	Sequence 18, Appl
42	30	66.7	1235	7	US-11-039-398-16	Sequence 16, Appl
43	30	66.7	1249	7	US-11-039-398-22	Sequence 22, Appl
44	30	66.7	1252	7	US-11-039-398-20	Sequence 20, Appl
45	30	66.7	1552	6	US-10-330-773-941	Sequence 941, App

ALIGNMENTS

RESULT 1
US-11-010-748A-11

; Sequence 11, Application US2005024421A1
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-11

Query Match   100.0%; Score 45; DB 7; Length 9;
Best Local Similarity   100.0%;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
              |||||||||
Db   1 VLHDDLLEA 9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: Patentin version 3.1

SEQ ID NO 12
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(9)
OTHER INFORMATION:
OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c...
US-11-010-748A-12

Query Match   82.2%; Score 37; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+05;
Matches   8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy  1 VLHDDLLEA 9
      || ||||||
Db  1 VLRDDLLEA 9
```

RESULT 3
US-11-087-099-5406
Sequence 5406, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 5406
LENGTH: 519
TYPE: PRT
ORGANISM: Candida apicola
US-11-087-099-5406

Query Match   73.3%; Score 33; DB 7; Length 519;
Best Local Similarity 75.0%; Pred. No. 69;
Matches   6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 VLHDDLLE  8
        |||| |||
Db  63 MLHDNLLE 70
```

RESULT 4
US-11-087-099-9352
Sequence 9352, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9352
LENGTH: 519
TYPE: PRT
ORGANISM: Candida apicola
US-11-087-099-9352

Query Match   73.3%; Score 33; DB 7; Length 519;
Best Local Similarity 100.0%; Pred. No. 69;
Matches   6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   3 HDDLLE  8
       ||||||
Db  65 HDDLLE 70
```

RESULT 5
US-10-793-626-1068
Sequence 1068, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1068
LENGTH: 623
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-1068

Query Match   73.3%; Score 33; DB 6; Length 623;
Best Local Similarity 66.7%; Pred. No. 85;
Matches   6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy    1 VLHDDLLEA   9
        | ||| ||||
Db  606 VVHDKLLEA 614
```

RESULT 6
US-11-092-140-9
Sequence 9, Application US/11092140
Publication No. US20050262590A1
GENERAL INFORMATION:
APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y.
TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthes...
FILE REFERENCE: 16515.054
CURRENT APPLICATION NUMBER: US/11/092,140
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: US/09/688,069
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 9
LENGTH: 297
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-11-092-140-9

Query Match   71.1%; Score 32; DB 7; Length 297;
Best Local Similarity 62.5%; Pred. No. 58;
Matches   5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 VLHDDLLE  8
        ||| ||:|
Db  77 LLHDDVLD 84
```

RESULT 7
US-11-092-140-12
Sequence 12, Application US/11092140
Publication No. US20050262590A1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 21:44:02 ; Search time 79 Seconds
                 (without alignments)
                 50.056 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLRA 9
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   A_Geneseq_21:*
             1: geneseqp1980s:*
             2: geneseqp1990s:*
             3: geneseqp2000s:*
             4: geneseqp2001s:*
             5: geneseqp2002s:*
             6: geneseqp2003as:*
             7: geneseqp2003bs:*
             8: geneseqp2004s:*
             9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	2	AAW99196	Aaw99196 Minor his
2	45	100.0	9	2	AAW97375	Aaw97375 HA-1 H-al
3	45	100.0	9	8	ADH40333	Adh40333 Human min
4	37	82.2	9	2	AAW99197	Aaw99197 Minor his
5	37	82.2	9	2	AAW97374	Aaw97374 HA-1 R-al
6	37	82.2	9	8	ADH40334	Adh40334 Human min
7	36	80.0	9	2	AAW99195	Aaw99195 Minor his
8	36	80.0	9	2	AAW97572	Aaw97572 T-cell ep
9	31	68.9	9	8	ADU99853	Adu99853 BC24 tumo
10	30	66.7	9	2	AAW97373	Aaw97373 Peptide e
11	28	62.2	9	2	AAY10122	Aay10122 T cell ep
12	28	62.2	9	5	ABG79805	Abg79805 MHC class
13	28	62.2	9	8	ADK68732	Adk68732 Epitope 1
14	28	62.2	9	8	ADK05291	Adk05291 Hepatitis
15	28	62.2	9	8	ADK05293	Adk05293 Hepatitis
16	28	62.2	9	8	ADQ10530	Adq10530 Cercopith
17	28	62.2	9	8	ADS81010	Ads81010 Tumour-as
18	27	60.0	9	8	ABJ20115	Abj20115 MHC bindi
19	27	60.0	9	9	ADT02787	Adt02787 Human tum
20	27	60.0	9	8	ABU97232	Abu97232 Enzyme pe
21	26	57.8	9	8	ABU97233	Abu97233 Enzyme pe
22	26	57.8	9	8	ABU97234	Abu97234 Enzyme pe
23	26	57.8	9	8	ABU97231	Abu97231 Enzyme pe
24	26	57.8	9	9	ADY63770	Ady63770 Human alb
25	26	57.8	8	7	ADM96262	Adm96262 Human ser
26	26	57.8	9	5	AAE31275	Aae31275 Human mag
27	26	57.8	9	8	ADM96261	Adm96261 Human ser
28	26	57.8	9	8	ADM96258	Adm96258 Human ser
29	26	57.8	9	8	ADT73023	Adt73023 Human RSV
30	26	57.8	9	8	ADT49074	Adt49074 Human BFA
31	26	57.8	9	8	ADU99636	Adu99636 BFA5 tumo
32	26	55.6	9	8	ADU97229	Adu97229 Enzyme pe
33	25	55.6	9	6	ABU97230	Abu97230 Enzyme pe
34	25	55.6	9	4	AAG79144	Aag79144 Amino ter
35	25	55.6	9	9	AAB84492	Aab84492 Peptide f
36	25	55.6	9	7	AAE26631	Aae26631 Yeast GPA
37	25	55.6	9	2	ADC25689	Adc25689 Yeast GPA
38	24	53.3	9	6	AAR29358	Aar29358 Endotheli
39	24	53.3	9	6	AAR69140	Aar69140 Endotheli
40	24	53.3	9	2	AAW33386	Aaw33386 Altered I
41	24	53.3	9	7	AAB70589	Aab70589 Human imm
42	24	53.3	9	4	AAO21066	Aao21066 Isomerise
43	24	53.3	9	5	AAE28095	Aae28095 Human imm
44	24	53.3	9	8	ADT39474	Adt39474 hSARS vir
45	24	53.3	9	8	ADS78093	Ads78093 SARS viru

ALIGNMENTS

RESULT 1
AAW99196

ID   AAW99196 standard; peptide; 9 AA.
AC   AAW99196;
XX
DT   20-MAY-1999 (first entry)
XX
DB   Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
DR   WPI; 1999-153312/13.
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998; 98WO-NL000425.
XX
PR   23-JUL-1997; 97EP-00202303.
XX
PA   (UYLR-) RIJKSUNIV LEIDEN.
PI   Goulmy RAJM, Hunt DF, Engelhard VH;
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
PS   Claim 3; Page 32; 47pp; English.
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
SQ   Sequence 9 AA;

Query Match   100.0%;   Score 45; DB 2;   Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
           |||||||||
Db   1 VLHDDLLEA 9

RESULT 2
AAW97375
ID   AAW97375 standard; protein; 9 AA.
XX
AC   AAW97375;
XX
DT   13-MAY-1999 (first entry)
XX
DE   HA-1 H-allele sequence.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease; SS.
OS   Homo sapiens.
XX
PN   WO990S313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-0087012S.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy B;
XX
PS   Claim 18; Fig 5; 59pp; English.
XX
CC   The present sequence represents part of the minor histocompatibility
CC   antigen HA-1 H-allele. The specification describes methods for typing
CC   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
CC   of genetic aberrances.
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
CC   antigen HA-1, in a sample, which comprise detecting polymorphic
CC   alleles (preferably the H and R alleles) of the minor histocompatibility
CC   nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC   methods can be used for HA-1 typing for bone marrow transplants, severe
CC   aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC   detection of genetic aberrances. The probes and primers of the invention
CC   can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

Query Match   100.0%;   Score 45; DB 2;   Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
           |||||||||
Db   1 VLHDDLLEA 9

RESULT 3
ADH40333
ID   ADH40333 standard; peptide; 9 AA.
XX
AC   ADH40333;

XX
DT   11-MAR-2004 (first entry)
DE   Human minor histocompatibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocompatibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO200310669Z-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP0062S1.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERB) MERCK PATENT GMBH.
XX
PI   Strittmatter W, Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
XX   epitopes.
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

Query Match   100.0%;   Score 45; DB 8;   Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
           |||||||||
Db   1 VLHDDLLEA 9

RESULT 4
AAW99197
ID   AAW99197 standard; peptide; 9 AA.
XX
AC   AAW99197;
XX
DT   20-MAY-1999 (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: March 2, 2006, 21:44:37 ; Search time 20 Seconds
(without alignments)
43.298 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLRA 9
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621676 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	40.0	7	2	I46868	alpha-myosin heavy
2	17	37.8	9	2	S55696	phosphoenolpyruvat
3	16	35.6	7	2	PQ0663	membrane protein -
4	16	35.6	7	2	S68004	huolin, 75K chain
5	16	35.6	8	2	PC4131	hypothetical prote
6	15	33.3	6	2	S78764	ribosomal protein
7	15	33.3	7	2	A59489	protein kinase C i
8	14	31.1	7	2	S20446	elastase - Pseudom
9	14	31.1	8	2	XGHUEU	urine glycopeptide
10	14	31.1	8	2	A12872	transaldolase (EC
11	14	31.1	9	2	S10920	venom protein HR-3
12	14	31.1	9	2	A60427	macrophage cytotox
13	13	28.9	8	2	A61328	trypsin (EC 3.4.21
14	13	28.9	9	2	PH0942	T-cell receptor be
15	12	26.7	4	2	I40697	T-cell receptor be
16	12	26.7	5	2	PT0679	biotin A - Citroba
17	12	26.7	6	2	PT0601	T-cell receptor be
18	12	26.7	6	2	B35640	cerebellar degener
19	12	26.7	6	2	PT0533	T-cell receptor be
20	12	26.7	7	2	A34026	acetylcholinestera
21	12	26.7	7	2	B39040	calsequestrin, fas
22	12	26.7	7	2	PT0628	T-cell receptor be
23	12	26.7	7	2	PT0722	T-cell receptor be
24	12	26.7	7	2	PT0576	T-cell receptor be
25	12	26.7	7	2	PT0368	Ig gamma chain C r
26	12	26.7	8	2	PN0043	T-cell receptor be
27	12	26.7	8	2	PT0557	T-cell receptor be
28	12	26.7	9	2	A6010B	exotoxin A - Strep
29	12	26.7	9	2	PW0002	chlorophyll a/b-bi
30	12	26.7	9	2	S65913	pyridine synthes
31	12	26.7	9	2	PH0108	late G1-69 protein
32	12	26.7	9	2	PT0562	T-cell receptor be
33	12	26.7	9	2	B30572	T-cell receptor be
34	11	24.4	5	2	C41225	copper resistance
35	11	24.4	5	2	T10954	hypothetical prote
36	11	24.4	6	2	T10779	phosphoglycerate t
37	11	24.4	6	2	T11779	158K exoantigen -
38	11	24.4	7	2	S25266	ferredoxin a2 - Ja
39	11	24.4	7	2	PT0246	Ig heavy chain CRD
40	11	24.4	8	2	S69165	p1lB protein - Esc
41	11	24.4	8	2	S66419	chitin-binding pro
42	11	24.4	8	2	B33099	158K exoantigen
43	11	24.4	8	2	S22428	ferredoxin a2 - Ja
44	11	24.4	9	2	A11497	tetrameric protein
45	11	24.4	9	2	B39504	octamer-binding pr

ALIGNMENTS

RESULT 1
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
R;Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventriculi
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: UNIPROT:Q28742; UNIPARC:UPI000087938; GB:K01698; NID:g165538; PIDN

Query Match 40.0%; Score 18; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDD 5
      |||:
Db 3 MHDB 6

RESULT 2
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55696
R;Hunt, M.; Koehler, P.
R;Biochim. Biophys. Acta 1249, 15-22, 1995
A;Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Tr
A;Reference number: S55696; MUID:95284106; PMID:7766679
A;Accession: S55696
A;Molecule type: protein
A;Status: preliminary
A;Residues: 1-9 <HUN>
A;Cross-references: UNIPROT:Q7M3S5; UNIPARC:UPI000017B599

Query Match 37.8%; Score 17; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDL 6
      :|| :|
Db 3 IIHKNL 8

RESULT 3
PQ0663

```
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C;Species: porcine epidemic diarrhea virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C;Accession: PQ0663
J.Gen.Virol. 74, 1795-1804, 1993
R;Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
issible gastroenteritis virus.
A;Reference number: JO2191; MUID:9389433; PMID:8397280
A;Accession: PQ0663
A;Molecule type: mRNA
A;Residues: 1-7 <BRI>
C;Cross-references: UNIPARC:UPI0000170PAC; GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:
C;Comment: This virus is coronavirus related to human coronavirus 229E.
C;Keywords: membrane protein

          Query Match    35.6%;  Score 16;  DB 2;  Length 7;
          Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
          Matches   3;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1  VLH 3
            |||
Db       3  VLH 5
```

```
RESULT 4
S68004
hucolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A;Reference number: S68004; MUID:96087107; PMID:7498469
A;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>
A;Cross-references: UNIPARC:UPI000017C164

          Query Match    35.6%;  Score 16;  DB 2;  Length 7;
          Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
          Matches   3;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       4  DDL 6
            |||
Db       4  DDL 6
```

```
RESULT 5
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: PC4131
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding
y for biosynthesis of heme d1.
A;Reference number: JC4552; MUID:96144254; PMID:8566817
A;Accession: PC4131
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-8 <KAW>
A;Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:g1217594
A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
C;Superfamily: Pseudomonas stutzeri nirD protein

          Query Match    35.6%;  Score 16;  DB 2;  Length 8;
          Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
          Matches   3;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
Qy       4  DDL 6
            |||
Db       2  DDL 4

RESULT 6
S78764
ribosomal protein MRP-S23, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78764
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Residues: 1-6 <GRA>
A;Cross-references: UNIPARC:UPI000017C570
A;Accession: S78764
A;Reference number: S78764
A;Accession: S78760
A;Molecule type: protein
C;Keywords: mitochondrion
F;1-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>

          Query Match    33.3%;  Score 15;  DB 2;  Length 6;
          Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
          Matches   3;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       2  LHDD 5
            |  ||
Db       1  LHVD 4
```

```
RESULT 7
A59489
protein kinase C inhibitor - rat (fragment)
C;Species: Rattus norvegicus
C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C;Accession: A59489
R;Negoro, M.
submitted to the Protein Sequence Database, June 2003
A;Description: Purification of PKCI from rat liver.
A;Reference number: A59489
A;Accession: A59489
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <NEG>
A;Experimental source: strain Wistar, liver
A;Note: p-Hydroxyacetophenone-Sepharose binding protein

          Query Match    33.3%;  Score 15;  DB 2;  Length 7;
          Best Local Similarity   40.0%;  Pred. No. 2.8e+05;
          Matches   2;  Conservative   1;  Mismatches   2;  Indels   0;  Gaps   0;

Qy       1  VLHDD 5
            |||
Db       2  IFEDD 6
```

```
RESULT 8
S20446
elaatase - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C;Accession: S20446
R;Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
FEBS Lett. 299, 291-293, 1992
A;Title: Identification of cleavage sites involved in proteolytic processing of Pseudomo
A;Reference number: S20446; MUID:92183956; PMID:1544509
A;Accession: S20446
A;Molecule type: protein
A;Status: preliminary
A;Residues: 1-7 <KES>
A;Cross-references: UNIPARC:UPI000017A95F

          Query Match    31.1%;  Score 14;  DB 2;  Length 7;
```

```
OM protein - protein search, using sw model
                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Bioacceleration Ltd.

Run on:             March  2, 2006, 21:44:22 ; Search time 99 seconds
                                              (without alignments)
                    64.139 Million cell updates/sec

Title:              US-10-623-176A-2
Perfect score:      45
Sequence:           1 VLHDDLLEA 9

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           2166443 segs, 70528306 residues .

Total number of hits satisfying chosen parameters:   1766

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  UniProt_05.80:*
            1: uniprot_sprot:*
            2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	19	42.2	9	2	Q7R8X5_PLAYO	plasmodium
2	19	42.2	9	2	Q47556_ECOLI	escherichia
3	18	40.0	9	7	Q28742_RABIT	oryctolagus
4	17	37.8	9	2	Q7m3s5_9TRYP	trypanosoma
5	16	35.6	9	2	O99182_9SMBG	gnatholebia
6	16	35.6	7	2	Q72sg0_HUMAN	homo sapien
7	16	35.6	9	1	PA88_MACRS	macrobrachi
8	16	35.6	9	2	P83281	macrobrachi
9	16	35.6	9	2	Q70SM2_HUMAN	homo sapien
10	16	35.6	9	2	Q4X981_PLACH	plasmodium
11	16	35.6	9	2	Q8LPT5_MAIZE	zea mays (m
12	16	35.6	8	2	P82568_STRPY	streptococc
13	15	33.3	8	2	O15900_HUMAN	homo sapien
14	15	33.3	9	2	Q4XT27_PLACH	plasmodium
15	15	33.3	6	1	Q9XJN0_9VIRU	bacteriopha
16	15	33.3	6	1	TRP1_PSEPU	pseudomonas
17	14	31.1	8	1	GLUR_HUMAN	homo sapien
18	14	31.1	8	2	Q9BFA7_MACPR	macroscelid
19	14	31.1	8	2	P72279_RHOGO	rhodococcus
20	14	31.1	8	2	Q93SR0_STARP	staphylococ
21	14	31.1	9	1	TAL1_PICJA	pichia jadi
22	14	31.1	9	2	Q7M4R5_HUMAN	homo sapien
23	14	31.1	9	2	Q7M471_VESOR	vespa orien
24	14	31.1	9	2	Q9FS22_CICAR	cicer ariet
25	14	31.1	9	2	Q8CG39_RAT	rattus norv
26	14	31.1	9	2	Q9QZA8_MOUSE	mus musculu
27	14	31.1	9	2	Q607G0_RANRI	rana ridibu
28	14	31.1	9	2	O85710_9RETR	rous sarcom
29	13	28.9	7	2	Q8UTD7_9HIV1	human immun
30	13	28.9	8	2	O62205_9CORO	transmissib
31	13	28.9	8	2	Q9HDS4_ASPFL	aspergillus
32	13	28.9	8	2	Q7M390_BALAC	balaenopter
33	13	28.9	8	2	Q37854_BPR17	bacteriopha
34	13	28.9	8	2	Q6JC68_SOYBN	glycine max
35	13	28.9	8	2	Q7XBD3_MAIZE	zea mays (m
36	13	28.9	8	2	Q51594_9ZZZZ	plasmid col
37	13	28.9	9	2	Q6UVK2_MALDO	malus domes
38	13	28.9	9	2	Q7X8P7_MAIZE	zea mays (m
39	13	28.9	9	2	Q56889_SAMCA	sambucus ca
40	13	28.9	9	2	Q56ST0_9DIPS	viburnum ut
41	13	28.9	9	2	Q56ST1_9DIPS	viburnum ur
42	13	28.9	9	2	Q56ST2_9DIPS	viburnum tr
43	13	28.9	9	2	Q56ST3_VIBOP	viburnum op
44	13	28.9	9	2	Q56ST4_9DIPS	viburnum ti
45	13	28.9	9	2	Q56ST5_9DIPS	viburnum su

ALIGNMENTS

RESULT 1
Q7R8X5_PLAYO
```
ID   Q7R8X5_PLAYO PRELIMINARY;    PRT;     9 AA.
AC   Q7R8X5;
DT   01-MAR-2004 (TrEMBlrel. 26, Created)
DT   01-MAR-2004 (TrEMBlrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBlrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=PY07095;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=17XNL;
RX   MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01002528; EAA19452.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   9 AA;  1013 MW;  4684D4472444441E7 CRC64;

     Query Match             42.2%;  Score 19;  DB 2;  Length 9;
     Best Local Similarity   50.0%;
     Matches    3;  Conservative   3;  Mismatches   0;  Indels   0;  Gaps   0;
                                      Pred. No. 2.2e+06;

Qy          1 VLHDDL 6
              :|:||:
Db          1 MLHNNL 6
```

RESULT 2
Q47556_ECOLI
```
ID   Q47556_ECOLI PRELIMINARY;    PRT;     9 AA.
AC   Q47556;
DT   01-NOV-1996 (TrEMBlrel. 01, Created)
DT   01-NOV-1996 (TrEMBlrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBlrel. 08, Last annotation update)
DE   Aspartate transcarbamoylase regulatory chain (Fragment).
GN   Name=pyrI;
```

```
OS   Escherichia coli K12.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83333;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82275057; PubMed=7051000;
RA   Pauza C.D., Karels M.J., Navre M., Schachman H.K.;
RT   "Genes encoding Escherichia coli aspartate transcarbamoylase: the
RT   pyrB-pyrI operon.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83195078; PubMed=6302686;
RA   Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
RA   Wild J.R.;
RT   "Nucleotide sequence of the structural gene (pyrB) that encodes the
RT   catalytic polypeptide of aspartate transcarbamoylase of Escherichia
RT   coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
DR   EMBL; J01670; AAA24475.1; -; Genomic_DNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1085 MW;  99EFD723344AA1F1 CRC64;

Qy   3 HDDLLE 8
       ||:.|:
Db   3 HDNKLQ 8

Query Match             42.2%;   Score 19;  DB 2;  Length 9;
Best Local Similarity   50.0%;   Pred. No. 2.2e+06;
Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;


RESULT 3
ID   Q28742_RABIT     PRELIMINARY;      PRT;     7 AA.
AC   Q28742;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-myosin heavy chain (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84221901; PubMed=6328491;
RA   Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.J., Jokovcic S.,
RA   Rabinowitz M.;
RT   "Characterization of genomic clones specifying rabbit alpha- and beta-
RT   ventricular myosin heavy chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR   EMBL; K01698; AAA31415.1; -; Genomic_DNA.
DR   PIR; I46868; I46868.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  916 MW;  6B1B1AA1B69326B0 CRC64;

Qy   2 LHDD 5
       :||:
Db   3 MHDE 6

Query Match             40.0%;   Score 18;  DB 2;  Length 7;
Best Local Similarity   50.0%;   Pred. No. 2.2e+06;
Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 4
ID   Q7M3S5_9TRYP     PRELIMINARY;      PRT;     9 AA.
AC   Q7M3S5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phosphoenolpyruvate carboxykinase.
OS   Trypanosoma brucei.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN   [1]
OX   NCBI_TaxID=5691;
RP   PROTEIN SEQUENCE.
RX   MEDLINE=95284106; PubMed=7766679; DOI=10.1016/0167-4838(95)00061-X;
RA   Hunt M., Koehler P.;
RT   "Purification and characterization of phosphoenolpyruvate
RT   carboxykinase from Trypanosoma brucei.";
RL   Biochim. Biophys. Acta 1249:15-22(1995).
DR   PIR; S55696; S55696.
SQ   SEQUENCE   9 AA;  1063 MW;  35F2D4431B05047 CRC64;

Qy   1 VLHDDLL 7
       ::|:||
Db   3 IIHKNL 8

Query Match             37.8%;   Score 17;  DB 2;  Length 9;
Best Local Similarity   33.3%;   Pred. No. 2.2e+06;
Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;


RESULT 5
ID   O99182_9SMEG     PRELIMINARY;      PRT;     7 AA.
AC   O99182;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Cytochrome oxidase I (Fragment).
GN   Name=COI;
OS   Gnatholebias zonatus.
OS   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Cyprinodontiformes; Aplocheiloidei; Rivulidae; Rivulinae; Gnatholebias.
OG   Mitochondrion.
OX   NCBI_TaxID=135316;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20072928; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
RA   Murphy W.J., Thomerson J.E., Collier G.E.;
RT   "Phylogeny of the Neotropical killifish family Rivulidae
RT   (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT   sequences.";
RL   Mol. Phylogenet. Evol. 13:289-301(1999).
DR   EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  899 MW;  672721F6CB572030 CRC64;

Qy   1 VLHDDLL 7
       :|:.||
Db   1 ILYQHLL 7

Query Match             35.6%;   Score 16;  DB 2;  Length 7;
Best Local Similarity   42.9%;   Pred. No. 2.2e+06;
Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;


RESULT 6
ID   Q726G0_HUMAN     PRELIMINARY;      PRT;     8 AA.
AC   Q726G0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fumarate hydratase (Fragment).
OS   Homo sapiens (Human).
```

```
OM protein - protein search, using sw model

                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Bioacceleration Ltd.

Run on:             March 2, 2006, 21:45:17 ; Search time 25 Seconds
                                               (without alignments)
                                               29.763 Million cell updates/sec

Title:              US-10-623-176A-2
Perfect score:      45
Sequence:           1 VLHDDLLEA 9
Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched:           572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:     111694

Minimum DB seq length: 0
Maximum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :          Issued_Patents_AA:*
                    1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                    2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                    3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                    4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
                    6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES

Result          Query
No.    Score    Match  Length  DB  ID                  Description
-----  -----    -----  ------  --  --                  -----------
1      45       100.0    9     2   US-09-269-250B-20   Sequence 20, Appl
2      45       100.0    9     2   US-09-489-760-2     Sequence 2, Appli
3      37       82.2     9     2   US-09-269-250B-18   Sequence 18, Appl
4      37       82.2     9     2   US-09-489-760-5     Sequence 5, Appli
5      36       80.0     9     2   US-09-269-250B-29   Sequence 29, Appl
6      36       80.0     9     2   US-09-489-760-1     Sequence 1, Appl
7      30       66.7     9     2   US-09-489-760-4     Sequence 4, Appli
8      30       66.7     8     2   US-09-269-250B-38   Sequence 38, Appli
9      28.5     63.3     8     2   US-09-269-250B-38   Sequence 38, Appli
10     25       55.6     7     2   US-09-025-819-5     Sequence 5, Appli
11     25       55.6     7     2   US-09-808-126-5     Sequence 5, Appl
12     25       55.6     9     2   US-09-803-951-5     Sequence 5, Appl
13     25       55.6     9     2   US-08-582-333A-3    Sequence 3, Appl
14     25       55.6     9     2   US-09-305-923A-7    Sequence 7, Appl
15     25       55.6     6     2   US-08-946-298-4     Sequence 4, Appl
16     23       51.1     6     2   US-09-217-609A-8    Sequence 8, Appl
17     23       51.1     6     2   US-08-873-235B-8    Sequence 8, Appli
18     23       51.1     5     2   US-08-159-339A-370  Sequence 370, App
19     22       48.9     5     2   US-08-811-463-30    Sequence 30, Appl
20     22       48.9     5     2   US-09-933-497B-30   Sequence 30, Appl
21     22       48.9     7     1   US-08-208-036-7     Sequence 7, Appl
22     22       48.9     7     1   US-08-208-036-9     Sequence 9, Appl
23     22       48.9     7     1   US-08-428-823-7     Sequence 7, Appli
24     22       48.9     7     1   US-08-428-823-9     Sequence 9, Appli
25     22       48.9     7     1   US-08-556-419-14    Sequence 14, Appl
26     22       48.9     7     2   US-09-173-941-82    Sequence 82, Appl
27     22       48.9     8     1   US-08-494-190-82    Sequence 82, Appl
28     22       48.9     9     2   US-08-403-378B-13   Sequence 13, Appl
29     22       48.9     9     2   US-09-217-609A-11   Sequence 11, Appl
30     21       46.7     6     1   US-08-873-235B-11   Sequence 11, Appl
31     21       46.7     6     2   US-08-459-568-20    Sequence 20, Appl
32     21       46.7     6     1   US-08-399-411-20    Sequence 20, Appl
33     21       46.7     6     2   US-08-516-859A-20   Sequence 20, Appl
34     21       46.7     6     2   US-09-586-472-20    Sequence 20, Appl
35     21       46.7     6     1   US-09-528-706-20    Sequence 20, Appl
36     21       46.7     8     2   US-08-459-568-75    Sequence 75, Appl
37     21       46.7     8     2   US-08-399-411-75    Sequence 75, Appl
38     21       46.7     8     2   US-09-419-826-1     Sequence 1, Appl
39     21       46.7     8     2   US-09-419-826-37    Sequence 37, Appl
40     21       46.7     8     2   US-09-586-472-75    Sequence 75, Appl
41     21       46.7     8     1   US-09-528-706-75    Sequence 75, Appl
42     21       46.7     8     2   US-07-671-757-30    Sequence 30, Appl
43     21       46.7     9     1   US-08-343-602-2     Sequence 2, Appli
44     21       46.7     9     2   US-08-459-568-72    Sequence 72, Appli
45     21       46.7     8     1   US-08-459-568-78    Sequence 78, Appl

                            ALIGNMENTS

RESULT 1
US-09-269-250B-20
; Sequence 20, Application.US/09269250B
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250B
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250B-20

Query Match     100.0%;  Score 45; DB 2; Length 9;
Best Local Similarity  100.0%;
Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9

RESULT 2
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
```

US-09-489-760-2
Query Match   100.0%;   Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
       |||||||||
Db 1 VLHDDLLEA 9

RESULT 3
US-09-269-250E-18
; Sequence 18, Application US/0926925OE
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments

Query Match   82.2%;   Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
       || |||||||
Db 1 VLRDDLLEA 9

RESULT 4
US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA

Query Match   82.2%;   Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
       || |||||||
Db 1 VLRDDLLEA 9

RESULT 5

US-09-269-250E-29
; Sequence 29, Application US/0926925OE
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue

Query Match   80.0%;   Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
       || |||||||
Db 1 VLXDDLLEA 9

RESULT 6
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
; OTHER INFORMATION: RESIDUE

Query Match   80.0%;   Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
       || |||||||
Db 1 VLXDDLLEA 9

RESULT 7
US-09-489-760-4
; Sequence 4, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006   Bioacceleration Ltd.

Run on: March   2, 2006, 21:46:48 ; Search time 42 Seconds
                                              (without alignments)
                                              89.535 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
•Maximum•DB•seq•length•=•0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA Main:*
                  1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                  2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                  3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                  4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                  5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	4	US-10-623-176-2	Sequence 2, Appli
2	45	100.0	9	4	US-10-791-217-2	Sequence 2, Appli
3	45	100.0	9	5	US-10-861-335-1	Sequence 1, Appl
4	45	100.0	9	6	US-11-007-740-20	Sequence 20, Appl
5	41	91.1	9	4	US-10-623-176-41	Sequence 41, Appl
6	41	91.1	9	4	US-10-623-176-45	Sequence 45, Appl
7	37	82.2	9	4	US-10-623-176-10	Sequence 10, Appl
8	37	82.2	9	4	US-10-623-176-47	Sequence 47, Appl
9	37	82.2	9	4	US-10-623-176-5	Sequence 5, Appl
10	37	82.2	9	4	US-11-007-740-18	Sequence 18, Appl
11	36	80.0	9	4	US-10-623-176-1	Sequence 1, Appl
12	36	80.0	9	4	US-10-623-176-40	Sequence 40, Appl
13	36	80.0	9	4	US-10-791-217-1	Sequence 1, Appl
14	36	80.0	9	6	US-11-007-740-29	Sequence 29, Appl
15	33	73.3	9	4	US-10-623-176-42	Sequence 42, Appl
16	33	73.3	9	4	US-10-623-176-46	Sequence 46, Appl
17	32	71.1	9	4	US-10-623-176-4	Sequence 4, Appl
18	30	66.7	9	4	US-10-623-176-14	Sequence 14, Appl
19	30	66.7	9	4	US-10-791-217-4	Sequence 4, Appl
20	30	66.7	9	5	US-11-007-740-40	Sequence 40, Appl
21	29	64.4	9	4	US-10-623-176-48	Sequence 48, Appl
22	28.5	63.3	8	4	US-10-623-176-15	Sequence 15, Appl
23	28.5	63.3	8	6	US-10-623-740-38	Sequence 38, Appl
24	28	62.2	9	4	US-10-623-176-23	Sequence 23, Appl
25	28	62.2	9	4	US-10-623-176-38	Sequence 38, Appl
26	28	62.2	9	4	US-10-777-053-95	Sequence 95, Appl
27	28	62.2	9	4	US-10-837-217-95	Sequence 95, Appl
28	27	60.0	9	5	US-10-705-459-280	Sequence 280, App
29	26	57.8	6	4	US-10-166-225A-163	Sequence 163, App
30	26	57.8	6	4	US-10-166-225A-164	Sequence 164, App
31	26	57.8	6	4	US-10-166-225A-165	Sequence 165, App
32	26	57.8	6	4	US-10-166-225A-166	Sequence 166, App
33	26	57.8	6	5	US-10-825-026-48	Sequence 48, Appl
34	25	55.6	6	4	US-10-166-225A-161	Sequence 161, App
35	25	55.6	6	4	US-10-166-225A-162	Sequence 162, App
36	25	55.6	7	5	US-09-803-951-5	Sequence 5, Appli
37	25	55.6	3	5	US-09-747-774A-3	Sequence 3, Appli
38	25	55.6	3	5	US-09-953-354-3	Sequence 3, Appli
39	25	55.6	9	3	US-10-267-074-14	Sequence 14, Appl
40	25	55.6	9	4	US-10-267-074-16	Sequence 16, Appl
41	25	55.6	9	5	US-10-752-478-3	Sequence 3, Appli
42	25	55.6	9	5	US-10-967-087-4	Sequence 4, Appli
43	24	53.3	7	4	US-10-020-354-86	Sequence 86, Appl
44	24	53.3	8	5	US-10-808-187-462	Sequence 462, App
45	24	53.3	8	5	US-10-807-807-462	Sequence 462, App

ALIGNMENTS

RESULT 1
US-10-623-176-2

; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-60447US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR APPLICATION NUMBER: 2000-01-21
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

  Query Match   100.0%; Score 45; DB 4; Length 9;
  Best Local Similarity   100.0%;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
              |||||||||
Db   1 VLHDDLLEA 9

RESULT 2
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H

TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

Query Match   100.0%; Score 45; DB 4; Length 9;
Best Local Similarity   100.0%; Pred. No. 1.7e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
           |||||||||
Db   1 VLHDDLLEA 9

RESULT 3
US-10-861-335-1
Sequence 1, Application US/10861335
Publication No. US20050031612A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
FILE REFERENCE: 2183-6479US
CURRENT APPLICATION NUMBER: US/10/861,335
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: PCT/NL02/00791
PRIOR FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: EP 01204704.9
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

Query Match   100.0%; Score 45; DB 5; Length 9;
Best Local Similarity   100.0%; Pred. No. 1.7e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
           |||||||||
Db   1 VLHDDLLEA 9

RESULT 4
US-11-007-740-20
Sequence 20, Application US/11007740
Publication No. US20050233350A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 2799/58994-A
CURRENT APPLICATION NUMBER: US/11/007,740
CURRENT FILING DATE: 2004-12-08
PRIOR APPLICATION NUMBER: 09/269,250
PRIOR FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

Query Match   100.0%; Score 45; DB 6; Length 9;
Best Local Similarity   100.0%; Pred. No. 1.7e+06;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
           |||||||||
Db   1 VLHDDLLEA 9

RESULT 5
US-10-623-176-41
Sequence 41, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-41

Query Match   91.1%; Score 41; DB 4; Length 9;
Best Local Similarity   100.0%; Pred. No. 1.7e+06;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEB 8
           ||||||||
Db   2 VLHDDLLE   9

RESULT 6
US-10-623-176-45
Sequence 45, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: March 2, 2006, 21:47:13 ; Search time 10 seconds
(without alignments)
18.000 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 35206

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Minimum DB seq length: 0
Maximum DB seq length: 0

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	100.0	45	9	7	US-11-010-748A-11	Sequence 11, Appl
2	82.2	37	9	7	US-11-010-748A-12	Sequence 12, Appl
3	57.8	26	9	7	US-11-019-027-5	Sequence 5, Appli
4	57.8	26	9	7	US-11-174-413-64	Sequence 64, Appl
5	57.8	26	9	7	US-11-129-143-164	Sequence 164, App
6	57.8	26	9	7	US-11-129-143-165	Sequence 165, App
7	55.8	25	9	7	US-11-129-143-166	Sequence 166, App
8	55.6	25	9	7	US-11-129-143-161	Sequence 161, App
9	55.6	25	9	7	US-11-129-143-162	Sequence 162, App
10	51.1	23	7	7	US-11-485-788A-353	Sequence 353, App
11	51.1	23	8	7	US-11-485-788A-354	Sequence 354, App
12	51.1	23	8	7	US-11-485-788A-355	Sequence 355, App
13	51.1	23	9	7	US-11-033-039-785	Sequence 785, App
14	51.1	23	9	5	US-11-033-039-809	Sequence 809, App
15	48.9	22	5	5	US-10-485-788A-443	Sequence 443, App
16	48.9	22	7	6	US-10-982-440-126	Sequence 126, App
17	48.9	22	8	7	US-11-045-024-444	Sequence 444, App
18	48.9	22	8	7	US-11-045-024-5467	Sequence 5467, App
19	48.9	22	8	7	US-11-045-024-7094	Sequence 7094, App
20	48.9	22	8	7	US-11-045-024-607	Sequence 607, App
21	48.9	22	9	7	US-11-045-024-3715	Sequence 3715, App
22	48.9	22	9	7	US-11-045-024-5511	Sequence 5511, Ap
23	48.9	22	9	7	US-11-045-024-12585	Sequence 12585, A
24	48.9	22	9	7	US-11-045-024-14029	Sequence 14029, A
25	46.7	21	4	6	US-10-485-788A-351	Sequence 351, App
26	44.4	20	4	6	US-10-667-295-263	Sequence 263, App
27	44.4	20	4	6	US-10-857-435A-366	Sequence 366, Appl
28	44.4	20	4	6	US-11-019-027-5	Sequence 5, Appli
29	44.4	20	4	7	US-11-174-413-64	Sequence 64, Appl
30	44.4	20	4	7	US-11-108-088-69	Sequence 69, Appl
31	44.4	20	5	7	US-11-129-143-168	Sequence 168, App
32	44.4	20	5	7	US-11-129-143-169	Sequence 169, App
33	44.4	20	5	7	US-11-129-143-170	Sequence 170, App
34	44.4	20	5	7	US-11-129-143-171	Sequence 171, App
35	44.4	20	5	7	US-11-129-143-172	Sequence 172, App
36	44.4	20	5	7	US-11-129-143-173	Sequence 173, App
37	44.4	20	5	7	US-10-857-435A-367	Sequence 367, App
38	44.4	20	6	7	US-10-857-435A-397	Sequence 397, App
39	44.4	20	6	7	US-10-857-435A-667	Sequence 667, App
40	44.4	20	8	7	US-11-021-305-62	Sequence 62, App
41	44.4	20	8	7	US-11-021-305-65	Sequence 65, App
42	44.4	20	8	7	US-11-021-305-66	Sequence 66, Appl
43	44.4	20	9	6	US-10-522-912-5	Sequence 5, Appli
44	44.4	20	9	6	US-10-522-912-8	Sequence 8, Appli
45	44.4	20	9	6	US-10-510-101-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c[...]
; OTHER INFORMATION: e11 epitopes
US-11-010-748A-11

Query Match   100.0%; Score 45; DB 7; Length 9;
Best Local Similarity   100.0%;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VLHDDLLEA 9
              |||||||||
Db   1 VLHDDLLEA 9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-12

Query Match   82.2%; Score 37; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 VLHDDLLEA 9
        | |||||||
Db   1 VLRDDLLEA 9

RESULT 3
US-11-129-143-163
; Sequence 163, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 163
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus

Query Match   57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   2 LHDDL 6
        ||||
Db   1 IHDDL 5

RESULT 4
US-11-129-143-164
; Sequence 164, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.

; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 164
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-129-143-164

Query Match   57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   2 LHDDL 6
        ||||
Db   1 IHDDL 5

RESULT 5
US-11-129-143-165
; Sequence 165, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 165
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-129-143-165

Query Match   57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   2 LHDDL 6
        ||||
Db   1 IHDDL 5

RESULT 6
US-11-129-143-166
; Sequence 166, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 166
; LENGTH: 6
; TYPE: PRT